



SEQUENCE LISTING

1) GENERAL INFORMATION:

- (i) APPLICANT: Soppet, Daniel R  
Yi, Li  
Rosen, Craig A  
Ruben, Steven
- (ii) TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
HLTDG74
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
Stewart & Olstein  
(B) STREET: 6 Becker Farm Road  
(C) CITY: Roseland  
(D) STATE: NJ  
(E) COUNTRY: USA  
(F) ZIP: 07068-1739
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/468,011  
(B) FILING DATE: 06-JUN-1995  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Ferraro, Gregory D  
(B) REGISTRATION NUMBER: 36,134  
(C) REFERENCE/DOCKET NUMBER: 325800-458
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 201-994-1700  
(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2003 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 90..1712
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GT	TT	TG	CT	CTG	GGC	AG	CCA	AAG	TT	GG	CAT	ATT	GGA	AG	CT	TTT	TCC	GG	GCT	CT	GG	AG	GAG	G	G	T		60
CC	CT	TG	CT	TCT	TC	CT	AC	AG	CC	GT	TCC	GG	GC	ATG	GCC	TGG	CTG	GGG	GCG	TCG	CTC							113
														Met	Ala	Trp	Leu	Gly	Ala	Ser	Leu							
														1				5										
CAC	GTC	TGG	GGT	TGG	CTA	ATG	CTC	GGC	AGC	TGC	CTC	CTG	GCC	AGA	GCC													161
His	Val	Trp	Gly	Trp	Leu	Met	Leu	Gly	Ser	Cys	Leu	Leu	Ala	Arg	Ala													
	10					15					20																	
CAG	CTG	GAT	TCT	GAT	GGC	ACC	ATC	ACT	ATA	GAG	GAG	CAG	ATT	GTC	CTT													209
Gln	Leu	Asp	Ser	Asp	Gly	Thr	Ile	Thr	Ile	Glu	Glu	Gln	Ile	Val	Leu													
	25				30					35					40													
GTG	CTG	AAA	GCG	AAA	GTA	CAA	TGT	GAA	CTC	AAC	ATC	ACA	GCT	CAA	CTC													257
Val	Leu	Lys	Ala	Lys	Val	Gln	Cys	Glu	Leu	Asn	Ile	Thr	Ala	Gln	Leu													
				45				50						55														
CAG	GAG	GGA	GAA	GGT	AAT	TGT	TTC	CCT	GAA	TGG	GAT	GGA	CTC	ATT	TGT													305
Gln	Glu	Gly	Glu	Gly	Asn	Cys	Phe	Pro	Glu	Trp	Asp	Gly	Leu	Ile	Cys													
				60				65					70															
TGG	CCC	AGA	GGA	ACA	GTG	GGG	AAA	ATA	TCG	GCT	GTT	CCA	TGC	CCT	CCT													353
Trp	Pro	Arg	Gly	Thr	Val	Gly	Lys	Ile	Ser	Ala	Val	Pro	Cys	Pro	Pro													
		75					80					85																
TAT	ATT	TAT	GAC	TTC	AAC	CAT	AAA	GGA	GTT	GCT	TTC	CGA	CAC	TGT	AAC													401
Tyr	Ile	Tyr	Asp	Phe	Asn	His	Lys	Gly	Val	Ala	Phe	Arg	His	Cys	Asn													
	90					95					100																	
CCC	AAT	GGA	ACA	TGG	GAT	TTT	ATG	CAC	AGC	TTA	AAT	AAA	ACA	TGG	GCC													449
Pro	Asn	Gly	Thr	Trp	Asp	Phe	Met	His	Ser	Leu	Asn	Lys	Thr	Trp	Ala													
	105				110					115					120													
AAT	TAT	TCA	GAC	TGC	CTT	CGC	TTT	CTG	CAG	CCA	GAT	ATC	AGC	ATA	GGA													497
Asn	Tyr	Ser	Asp	Cys	Leu	Arg	Phe	Leu	Gln	Pro	Asp	Ile	Ser	Ile	Gly													
				125				130						135														
AAG	CAA	GAA	TTC	TGT	GAA	CGC	CTC	TAT	GTA	ATG	TAT	ACC	GTT	GGC	TAC													545
Lys	Gln	Glu	Phe	Cys	Glu	Arg	Leu	Tyr	Val	Met	Tyr	Thr	Val	Gly	Tyr													
			140				145						150															
TCC	ATC	TCT	TTT	GGT	TCC	TTG	GCT	GTG	GCT	ATT	CTC	ATC	ATT	GGT	TAC													593
Ser	Ile	Ser	Phe	Gly	Ser	Leu	Ala	Val	Ala	Ile	Leu	Ile	Ile	Gly	Tyr													
		155				160						165																
TTC	AGA	CGA	TTG	CAT	TGC	ACT	AGG	AAC	TAT	ATC	CAC	ATG	CAC	TTA	TTT													641
Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe													
	170				175						180																	
GTG	TCT	TTT	ATG	CTG	AGA	GCT	ACA	AGC	ATC	TTT	GTC	AAA	GAC	AGA	GTA													689
Val	Ser	Phe	Met	Leu	Arg	Ala	Thr	Ser	Ile	Phe	Val	Lys	Asp	Arg	Val													
	185				190					195					200													
GTC	CAT	GCT	CAC	ATA	GGA	GTA	AAG	GAG	CTG	GAG	TCC	CTA	ATA	ATG	CAG													737
Val	His	Ala	His	Ile	Gly	Val	Lys	Glu	Leu	Glu	Ser	Leu	Ile	Met	Gln													
				205				210						215														
GAT	GAC	CCA	CAA	AAT	TCC	ATT	GAG	GCA	ACT	TCT	GTG	GAC	AAA	TCA	CAA													785
Asp	Asp	Pro	Gln	Asn	Ser	Ile	Glu	Ala	Thr	Ser	Val	Asp	Lys	Ser	Gln													
			220				225						230															
TAT	ATC	GGG	TGC	AAG	ATT	GCT	GTT	GTG	ATG	TTT	ATT	TAC	TTC	CTG	GCT													833

Tyr	Ile	Gly	Cys	Lys	Ile	Ala	Val	Val	Met	Phe	Ile	Tyr	Phe	Leu	Ala		
		235					240					245					
ACA	AAT	TAT	TAT	TGG	ATC	CTG	GTG	GAA	GGT	CTC	TAC	CTG	CAT	AAT	CTC	881	
Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His	Asn	Leu		
	250					255					260						
ATC	TTT	GTG	GCT	TTC	TTT	TCG	GAC	ACC	AAA	TAC	CTG	TGG	GGC	TTC	ATC	929	
Ile	Phe	Val	Ala	Phe	Phe	Ser	Asp	Thr	Lys	Tyr	Leu	Trp	Gly	Phe	Ile		
265				270					275						280		
TTG	ATA	GGC	TGG	GGG	TTT	CCA	GCA	GCA	TTT	GTT	GCA	GCA	TGG	GCT	GTG	977	
Leu	Ile	Gly	Trp	Gly	Phe	Pro	Ala	Ala	Phe	Val	Ala	Ala	Trp	Ala	Val		
				285					290					295			
GCA	CGA	GCA	ACT	CTG	GCT	GAT	GCG	AGG	TGC	TGG	GAA	CTT	AGT	GCT	GGA	1025	
Ala	Arg	Ala	Thr	Leu	Ala	Asp	Ala	Arg	Cys	Trp	Glu	Leu	Ser	Ala	Gly		
			300					305					310				
GAC	ATC	AAG	TGG	ATT	TAT	CAA	GCA	CCG	ATC	TTA	GCA	GCT	ATT	GGG	CTG	1073	
Asp	Ile	Lys	Trp	Ile	Tyr	Gln	Ala	Pro	Ile	Leu	Ala	Ala	Ile	Gly	Leu		
		315					320					325					
AAT	TTT	ATT	CTG	TTT	CTG	AAT	ACG	GTT	AGA	GTT	CTA	GCT	ACC	AAA	ATC	1121	
Asn	Phe	Ile	Leu	Phe	Leu	Asn	Thr	Val	Arg	Val	Leu	Ala	Thr	Lys	Ile		
	330					335					340						
TGG	GAG	ACC	AAT	GCA	GTT	GGG	CAT	GAC	ACA	AGG	AAG	CAA	TAC	AGG	AAA	1169	
Trp	Glu	Thr	Asn	Ala	Val	Gly	His	Asp	Thr	Arg	Lys	Gln	Tyr	Arg	Lys		
345				350					355					360			
CTG	GCC	AAA	TCG	ACA	CTG	GTC	CTG	GTC	CTA	GTC	TTT	GGA	GTG	CAT	TAC	1217	
Leu	Ala	Lys	Ser	Thr	Leu	Val	Leu	Val	Leu	Val	Phe	Gly	Val	His	Tyr		
				365					370					375			
ATC	GTG	TTC	GTG	TGC	CTG	CCT	CAC	TCC	TTC	ACT	GGG	CTC	GGG	TGG	GAG	1265	
Ile	Val	Phe	Val	Cys	Leu	Pro	His	Ser	Phe	Thr	Gly	Leu	Gly	Trp	Glu		
			380					385					390				
ATC	CGC	ATG	CAC	TGT	GAG	CTC	TTC	TTC	AAC	TCC	TTT	CAG	GGT	TTC	TTT	1313	
Ile	Arg	Met	His	Cys	Glu	Leu	Phe	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe		
		395					400					405					
GTG	TCT	ATC	ATC	TAC	TGC	TAC	TGC	AAT	GGA	GAG	GTT	CAG	GCA	GAG	GTG	1361	
Val	Ser	Ile	Ile	Tyr	Cys	Tyr	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Val		
	410					415					420						
AAG	AAG	ATG	TGG	AGT	CGG	TGG	AAT	CTC	TCC	GTG	GAC	TGG	AAA	AGG	ACA	1409	
Lys	Lys	Met	Trp	Ser	Arg	Trp	Asn	Leu	Ser	Val	Asp	Trp	Lys	Arg	Thr		
425				430					435					440			
CCG	CCA	TGT	GGC	AGC	CGC	AGA	TGC	GGC	TCA	GTG	CTC	ACC	ACC	GTG	ACG	1457	
Pro	Pro	Cys	Gly	Ser	Arg	Arg	Cys	Gly	Ser	Val	Leu	Thr	Thr	Val	Thr		
				445					450					455			
CAC	AGC	ACC	AGC	AGC	CAG	TCA	CAG	GTG	GCG	GCA	GCA	CAC	GCA	TGG	TGC	1505	
His	Ser	Thr	Ser	Ser	Gln	Ser	Gln	Val	Ala	Ala	Ala	His	Ala	Trp	Cys		
			460					465					470				
TTA	TCT	CTG	GCA	AAG	CTG	CCA	AGA	TCG	CCA	GCA	GAC	AGC	CTG	ACA	GCC	1553	
Leu	Ser	Leu	Ala	Lys	Leu	Pro	Arg	Ser	Pro	Ala	Asp	Ser	Leu	Thr	Ala		
		475					480					485					

ACA TCA UTT TAC CTG GCT ATG TCT GGA GTA ACT CAG AGC AGG ACT GCC 1601  
 Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala  
 490 495 500  
 TCA CAC ACT CTC TCC ACG AGG AGC AAC AAG GAA GAT AGT GGG AGG CAG 1649  
 Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln  
 505 510 515 520  
 AGA GAT GAT ATT CTA ATG GAG AAG CCT TCC AGG CCT ATG GAA TCT AAC 1697  
 Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn  
 525 530 535  
 CCA GAC ACT GAA GGA TGACAAGGAG AAAGTGAAGA TGTCTCTGA ATGGACATGT 1752  
 Pro Asp Thr Glu Gly  
 540  
 GTGGCTGACT TTCATGGGCT GGTCCAATGG CTGGTTGTGT GAGAGGGCTT GGCTGATACT 1812  
 CCTATGCTTG AGCACAAAGG CTGAAAATTC AGTTAAGGTG TTACTTAATA ATAGTTTTTA 1872  
 GGCTCCATGA ATTGGCTCCT GTAAATACTA ACGACATGAA AATGCAAGTG TCAATGGAGT 1932  
 AGTTTATTAC CTTCTATTGG CATCAAGTTT TCCTCTAAAT TAATGTATGG TATTTGCTCT 1992  
 GTGATTGTTC A 2003

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 541 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Trp Leu Gly Ala Ser Leu His Val Trp Gly Trp Leu Met Leu  
 1 5 10 15  
 Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile  
 20 25 30  
 Thr Ile Glu Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys  
 35 40 45  
 Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe  
 50 55 60  
 Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys  
 65 70 75 80  
 Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys  
 85 90 95  
 Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met  
 100 105 110  
 His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe  
 115 120 125  
 Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu

130

135

140

Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala  
 145 150 155 160  
 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg  
 165 170 175  
 Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Thr  
 180 185 190  
 Ser Ile Phe Val Lys Asp Arg Val Val His Ala His Ile Gly Val Lys  
 195 200 205  
 Glu Leu Glu Ser Leu Ile Met Gln Asp Asp Pro Gln Asn Ser Ile Glu  
 210 215 220  
 Ala Thr Ser Val Asp Lys Ser Gln Tyr Ile Gly Cys Lys Ile Ala Val  
 225 230 235 240  
 Val Met Phe Ile Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val  
 245 250 255  
 Glu Gly Leu Tyr Leu His Asn Leu Ile Phe Val Ala Phe Phe Ser Asp  
 260 265 270  
 Thr Lys Tyr Leu Trp Gly Phe Ile Leu Ile Gly Trp Gly Phe Pro Ala  
 275 280 285  
 Ala Phe Val Ala Ala Trp Ala Val Ala Arg Ala Thr Leu Ala Asp Ala  
 290 295 300  
 Arg Cys Trp Glu Leu Ser Ala Gly Asp Ile Lys Trp Ile Tyr Gln Ala  
 305 310 315 320  
 Pro Ile Leu Ala Ala Ile Gly Leu Asn Phe Ile Leu Phe Leu Asn Thr  
 325 330 335  
 Val Arg Val Leu Ala Thr Lys Ile Trp Glu Thr Asn Ala Val Gly His  
 340 345 350  
 Asp Thr Arg Lys Gln Tyr Arg Lys Leu Ala Lys Ser Thr Leu Val Leu  
 355 360 365  
 Val Leu Val Phe Gly Val His Tyr Ile Val Phe Val Cys Leu Pro His  
 370 375 380  
 Ser Phe Thr Gly Leu Gly Trp Glu Ile Arg Met His Cys Glu Leu Phe  
 385 390 395 400  
 Phe Asn Ser Phe Gln Gly Phe Phe Val Ser Ile Ile Tyr Cys Tyr Cys  
 405 410 415  
 Asn Gly Glu Val Gln Ala Glu Val Lys Lys Met Trp Ser Arg Trp Asn  
 420 425 430  
 Leu Ser Val Asp Trp Lys Arg Thr Pro Pro Cys Gly Ser Arg Arg Cys  
 435 440 445  
 Gly Ser Val Leu Thr Thr Val Thr His Ser Thr Ser Ser Gln Ser Gln  
 450 455 460  
 Val Ala Ala Ala His Ala Trp Cys Leu Ser Leu Ala Lys Leu Pro Arg



GTTGGCATAT TGGAAGCTTT TTGCGGG

27

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGTTTCTAG ATGTCATCCT TCAGTGTC

28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCCTACCCGG GCCGCCATCA TGGCCTGGCT GGGGGGCCT

39

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGTTTCTAG ATGTCATCCT TCAGTGTC

28